SEQUENCE LISTING

<110> Kroczek, Richard

<120> Anti-human T-cell costimulating monoclonal antibodies

<130> 7853-215-999

<140> 09/509,283
<141> 2000-08-11

<160> 5

<170> PatentIn version 3.0

<210> 1
<211> 2641
<212> DNA
<213> 8F4

<220>
<221> CDS
<222> 68..667

<400> 1

```
cgagagcctg aattcactgt cagctttgaa cactgaacgc gaggactgtt aactgtttct      60
ggcaaac atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc      109
        Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg
        1               5                  10
att aaa gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg      157
Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met
15                  20                  25                  30
ttt ata ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac      205
Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp
                35                  40                  45
att gtc cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc      253
Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu
            50                  55                  60
tgc gat ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag      301
Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys
        65                  70                  75
agt ctg aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt      349
Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe
    80                  85                  90
ttt cta tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac      397
Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn
95                  100                 105                 110
cta tca att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga      445
Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly
                115                 120                 125
tat ttg cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg      493
Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp
            130                 135                 140
tta ccc ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc      541
Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys
        145                 150                 155
ata ctt att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac      589
Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His
    160                 165                 170
gac cct aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa      637
Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys
175                 180                 185                 190
```

F10

```
aaa tct aga ctc aca gat gtg acc cta taa tatggaactc tggcacccag        687
Lys Ser Arg Leu Thr Asp Val Thr Leu
                195
gcatgaagca cgttggccag ttttcctcaa cttgaagtgc aagattctct tatttccggg    747
accacggaga gtctgactta actacataca tcttctgctg gtgttttgtt caatctggaa    807
gaatgactgt atcagtcaat ggggatttta acagactgcc ttggtactgc cgagtcctct    867
caaaacaaac accctcttgc aaccagcttt ggagaaagcc cagctcctgt gtgctcactg    927
ggagtggaat ccctgtctcc acatctgctc ctagcagtgc atcagccagt aaaacaaaca    987
catttacaag aaaaatgttt taaagatgcc aggggtactg aatctgcaaa gcaaatgagc   1047
agccaaggac cagcatctgt ccgcatttca ctatcatact acctcttctt tctgtaggga   1107
tgagaattcc tcttttaatc agtcaaggga gatgcttcaa agctggagct attttatttc   1167
tgagatgttg atgtgaactg tacattagta catactcagt actctccttc aattgctgaa   1227
ccccagttga ccattttacc aagactttag atgctttctt gtgccctcaa ttttcttttt   1287
aaaaatactt ctacatgact gcttgacagc ccaacagcca ctctcaatag agagctatgt   1347
cttacattct ttcctctgct gctcaatagt tttatatatc tatgcataca tatatacaca   1407
catatgtata taaaattcat aatgaatata tttgcctata ttctccctac aagaatattt   1467
ttgctccaga aagacatgtt cttttctcaa attcagttaa aatggtttac tttgttcaag   1527
ttagtggtag gaaacattgc ccggaattga aagcaaattt attttattat cctattttct   1587
accattatct atgttttcat ggtgctatta attacaagtt tagttctttt tgtagatcat   1647
attaaaattg caaacaaaat catctttaat gggccagcat tctcatgggg tagagcagaa   1707
tattcattta gcctgaaagc tgcagttact ataggttgct gtcagactat acccatggtg   1767
cctctgggct tgacaggtca aaatggtccc catcagcctg gagcagccct ccagacctgg   1827
gtggaattcc agggttgaga gactcccctg agccagaggc cactaggtat tcttgctccc   1887
agaggctgaa gtcaccctgg gaatcacagt ggtctacctg cattcataat tccaggatct   1947
gtgaagagca catatgtgtc agggcacaat tccctctcat aaaaaccaca cagcctggaa   2007
attggccctg gcccttcaag atagccttct ttagaatatg atttggctag aaagattctt   2067
aaatatgtgg aatatgatta ttcttagctg gaatattttc tctacttcct gtctgcatgc   2127
ccaaggcttc tgaagcagcc aatgtcgatg caacaacatt tgtaacttta ggtaaactgg   2187
gattatgttg tagtttaaca ttttgtaact gtgtgcttat agtttacaag tgagacccga   2247
tatgtcatta tgcatactta tattatctta agcatgtgta atgctggatg tgtacagtac   2307
agtactgaac ttgtaatttg aatctagtat ggtgttctgt tttcagctga cttggacaac   2367
ctgactggct ttgcacaggt gttccctgag ttgtttgcag gtttctgtgt gtggggtggg   2427
gtatggggag gagaaccttc atggtggccc acctggcctg gttgtccaag ctgtgcctcg   2487
acacatcctc atccccagca tgggacacct caagatgaat aataattcac aaaatttctg   2547
tgaaatcaaa tccagtttta agaggagcca cttatcaaag agattttaac agtagtaaga   2607
aggcaaagaa taaacatttg atattcagca actg                               2641
```

<210> 2
<211> 199
<212> PRT
<213> 8F4

<400> 2

```
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1               5                  10                  15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20                  25                  30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35                  40                  45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65                  70                  75                  80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95
```

F10

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 3
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Degenerate oligonucleotide

F10
<221> misc_feature
<222> 3, 9 , 15
<223> n = a, t, g, or c

<400> 3
mgnctsacng aygtnac 17

<210> 4
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Degenerate oligonucleotide

<221> misc_feature
<222> 3, 9 , 15
<223> n = a, t, g, or c

<400> 4
mgnytdacng aygtnac 17

<210> 5
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> 1
<223> Xaa = Unknown amino acid

<400> 5

F10

Xaa Arg Leu Thr Asp Val Thr
1 5